

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Genentech, Inc., Hsei, Vanessa
Koumenis, Iphigenia
Leong, Steven R.
Presta, Leonard G.
10 Shahrokh, Zahra
Zapata, Gerardo A.
- (ii) TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES
AND HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
- 15 (iii) NUMBER OF SEQUENCES: 72
- (iv) CORRESPONDENCE ADDRESS:
20 (A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080
- 25 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
30 (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 20-Jan-1999
35 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/074330
(B) FILING DATE: 22-JAN-1998
- 40 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/094003
(B) FILING DATE: 24-JUL-1998
- (vii) PRIOR APPLICATION DATA:
45 (A) APPLICATION NUMBER: 60/094013
(B) FILING DATE: 24-JUL-1998
- (vii) PRIOR APPLICATION DATA:
50 (A) APPLICATION NUMBER: 60/075467
(B) FILING DATE: 20-FEB-1998
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Love, Richard B.
55 (B) REGISTRATION NUMBER: 34,659
(C) REFERENCE/DOCKET NUMBER: P1085R4-1A

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-5530

(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGTCCAACT GTTCAGGACG CC 22

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGCTGCTCA TGCTGTAGGT GC 22

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAAGTTGATG TCTTGTGAGT GGC 23

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCATCCTAGA GTCACCGAGG AGCC 24

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CACTGGCTCA GGGAAATAAC CC 22

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGAGAGCTGG GAAGGTGTGC AC 22

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACAAACGCGT ACGCTGACAT CGTCATGACC CAGTC 35

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACAAACGCGT ACGCTGATAT TGTCATGACT CAGTC 35

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACAAACGCGT ACGCTGACAT CGTCATGACA CAGTC 35

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTCTTCGAA TGGTGGGAAG ATGGATACAG TTGGTGC 37

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGATGGGCCC GGATAGACCG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGATGGGCCC GGATAGACTG ATGGGGCTGT CGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGATGGGCCC GGATAGACGG ATGGGGCTGT TGTTTTGGC 39

5 (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: Nucleic Acid
 10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

15 CGATGGGCCC GGATAGACAG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:15:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

30 CGATGGGCCC GGATAGACTG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 base pairs
 35 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

40 GACATTGTCA TGACACAGTC TCAAAAATTC ATGTCCACAT CAGTAGGAGA 50
 CAGGGTCAGC GTCACCTGCA AGGCCAGTCA GAATGTGGGT ACTAATGTAG 100
 45 CCTGGTATCA ACAGAAACCA GGGCAATCTC CTAAAGCACT GATTTACTCG 150
 TCATCCTACC GGTACAGTGG AGTCCCTGAT CGCTTCACAG GCAGTGGATC 200
 50 TGGGACAGAT TTTACTCTCA CCATCAGCCA TGTGCAGTCT GAAGACTTGG 250
 CAGACTATTT CTGTCAGCAA TATAACATCT ATCCTCTCAC GTTCGGTCCT 300
 GGGACCAAGC TGGAGTTGAA ACGGGCTGAT GCTGCACCAC CAACTGTATC 350
 55 CATCTTCCCA CCATTCGAA 369

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asp	Ile	Val	Met	Thr	Gln	Ser	Gln	Lys	Phe	Met	Ser	Thr	Ser	Val	1	5	10	15
Gly	Asp	Arg	Val	Ser	Val	Thr	Cys	Lys	Ala	Ser	Gln	Asn	Val	Gly	20	25	30	
Thr	Asn	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	35	40	45	
Ala	Leu	Ile	Tyr	Ser	Ser	Ser	Tyr	Arg	Tyr	Ser	Gly	Val	Pro	Asp	50	55	60	
Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	65	70	75	
Ser	His	Val	Gln	Ser	Glu	Asp	Leu	Ala	Asp	Tyr	Phe	Cys	Gln	Gln	80	85	90	
Tyr	Asn	Ile	Tyr	Pro	Leu	Thr	Phe	Gly	Pro	Gly	Thr	Lys	Leu	Glu	95	100	105	
Leu	Lys	Arg	Ala	Asp	Ala	Ala	Pro	Pro	Thr	Val	Ser	Ile	Phe	Pro	110	115	120	
Pro	Phe	Glu													123			

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCTATTGCT	ACAAACGCGT	ACGCTGAGGT	GCAGCTGGTG	GAGTCTGGGG	50
GAGGCTTAGT	GCCGCCTGGA	GGGTCCCTGA	AACTCTCCTG	TGCAGCCTCT	100
GGATTCATAT	TCAGTAGTTA	TGGCATGTCT	TGGGTTCGCC	AGACTCCAGG	150
CAAGAGCCTG	GAGTTGGTCG	CAACCATTAA	TAATAATGGT	GATAGCACCT	200

ATTATCCAGA CAGTGTGAAG GGCCGATTCA CCATCTCCCG AGACAATGCC 250
 AAGAACACCC TGTACCTGCA AATGAGCAGT CTGAAGTCTG AGGACACAGC 300
 5 CATGTTTTAC TGTGCAAGAG CCCTCATTAG TTCGGCTACT TGGTTTGGTT 350
 ACTGGGGCCA AGGGACTCTG GTCAGTGTCT CTGCAGCCAA AACAACAGCC 400
 CCATCTGTCT ATCCGGG 417

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

20	Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Pro Pro Gly	15
	1 5 10	
	Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser	30
	20 25	
25	Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Gly Lys Ser Leu	45
	35 40	
30	Glu Leu Val Ala Thr Ile Asn Asn Asn Gly Asp Ser Thr Tyr Tyr	60
	50 55	
	Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala	75
	65 70	
35	Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp	90
	80 85	
	Thr Ala Met Phe Tyr Cys Ala Arg Ala Leu Ile Ser Ser Ala Thr	105
	95 100	
40	Trp Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala	120
	110 115	
45	Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro	130
	125	

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACAAACGCGT ACGCTGATAT CGTCATGACA G 31

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAGCATCAG CTCTTCGAAG CTCCAGCTTG G 31

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: DNA
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCACTAGTAC GCAAGTTCAC G 21

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATGGGCCCT TGGTGGAGGC TGCAGAGACA GTG 33

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 714 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT 50

TGCTACAAAC GCGTACGCTG ATATCGTCAT GACACAGTCT CAAAAATTCA 100

TGTCACATC AGTAGGAGAC AGGGTCAGCG TCACCTGCAA GGCCAGTCAG 150
 AATGTGGGTA CTAATGTAGC CTGGTATCAA CAGAAACCAG GGCAATCTCC 200
 TAAAGCACTG ATTTACTCGT CATCCTACCG GTACAGTGA GTCCCTGATC 250
 GCTTCACAGG CAGTGGATCT GGGACAGATT TCACTCTCAC CATCAGCCAT 300
 GTGCAGTCTG AAGACTTGGC AGACTATTTT TGTCAGCAAT ATAACATCTA 350
 TCCTCTCACG TTCGGTCCTG GGACCAAGCT GGAGCTTCGA AGAGCTGTGG 400
 CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT 450
 GGAAGTCTT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC 500
 CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG 550
 AGAGTGTAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC 600
 ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG 650
 CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA 700
 GGGGAGAGTG TTAA 714

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	20	25	30	
Gln	Lys	Phe	Met	Ser	Thr	Ser	Val	Gly	Asp	Arg	Val	Ser	Val	Thr	35	40	45	
Cys	Lys	Ala	Ser	Gln	Asn	Val	Gly	Thr	Asn	Val	Ala	Trp	Tyr	Gln	50	55	60	
Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Ala	Leu	Ile	Tyr	Ser	Ser	Ser	65	70	75	
Tyr	Arg	Tyr	Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	80	85	90	
Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	His	Val	Gln	Ser	Glu	Asp	95	100	105	

	Leu	Ala	Asp	Tyr	Phe	Cys	Gln	Gln	Tyr	Asn	Ile	Tyr	Pro	Leu	Thr	
					110					115					120	
5	Phe	Gly	Pro	Gly	Thr	Lys	Leu	Glu	Leu	Arg	Arg	Ala	Val	Ala	Ala	
					125					130					135	
	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	
10					140					145					150	
	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	
					155					160					165	
15	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	
					170					175					180	
	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	
					185					190					195	
20	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	
					200					205					210	
	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	
25					215					220					225	
	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
					230					235		237				

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 756 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

40	ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCTG TTTTCTCTAT	50
	TGCTACAAAC GCGTACGCTG AGGTGCAGCT GGTGGAGTCT GGGGGAGGCT	100
	TAGTGCCGCC TGGAGGGTCC CTGAAACTCT CCTGTGCAGC CTCTGGATTC	150
45	ATATTCAGTA GTTATGGCAT GTCTTGGGTT CGCCAGACTC CAGGCAAGAG	200
	CCTGGAGTTG GTCGCAACCA TTAATAATAA TGGTGATAGC ACCTATTATC	250
50	CAGACAGTGT GAAGGGCCGA TTCACCATCT CCCGAGACAA TGCCAAGAAC	300
	ACCCTGTACC TGCAAATGAG CAGTCTGAAG TCTGAGGACA CAGCCATGTT	350
	TTACTGTGCA AGAGCCCTCA TTAGTTCGGC TACTTGGTTT GGTTACTGGG	400
55	GCCAAGGGAC TCTGGTCACT GTCTCTGCAG CCTCCACCAA GGGCCCATCG	450

GTCTTCCCC TGGCACCCCTC CTCCAAGAGC ACCTCTGGGG GCACAGCGGC 500
 CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG ACGGTGTCGT 550
 5 GGAAGTCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCCTA 600
 CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG 650
 10 CAGCTTGGGC ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA 700
 ACACCAAGGT GGACAAGAAA GTTGAGCCCA AATCTTGTGA CAAAACCTCAC 750
 ACATGA 756

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

25	Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	
	1				5					10					15	
	Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Val	Gln	Leu	Val	Glu	Ser	
				20					25					30		
30	Gly	Gly	Gly	Leu	Val	Pro	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	
				35					40					45		
	Ala	Ala	Ser	Gly	Phe	Ile	Phe	Ser	Ser	Tyr	Gly	Met	Ser	Trp	Val	
35				50					55					60		
	Arg	Gln	Thr	Pro	Gly	Lys	Ser	Leu	Glu	Leu	Val	Ala	Thr	Ile	Asn	
				65					70					75		
40	Asn	Asn	Gly	Asp	Ser	Thr	Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	
				80					85					90		
	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	
				95					100					105		
45	Met	Ser	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Met	Phe	Tyr	Cys	Ala	
				110					115					120		
	Arg	Ala	Leu	Ile	Ser	Ser	Ala	Thr	Trp	Phe	Gly	Tyr	Trp	Gly	Gln	
50				125					130					135		
	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
				140					145					150		
55	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	
				155					160					165		

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
170 175 180

5 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
185 190 195

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
200 205 210

10 Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
215 220 225

15 Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
230 235 240

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
245 250 251

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCAATGCATA CGCTGACATC GTGATGACCC AGACCCC 37

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCAATGCATA CGCTGATATT GTGATGACTC AGACTCC 37

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCAATGCATA CGCTGACATC GTGATGACAC AGACACC 37

(2) INFORMATION FOR SEQ ID NO:31:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGATGTCAAT TGCTCACTGG ATGGTGGGAA GATGG 35

15 (2) INFORMATION FOR SEQ ID NO:32:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAAACGCGTA CGCTGAGATC CAGCTGCAGC AG 32

30 (2) INFORMATION FOR SEQ ID NO:33:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

40 CAAACGCGTA CGCTGAGATT CAGCTCCAGC AG 32

(2) INFORMATION FOR SEQ ID NO:34:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATATCGTGA TGACACAGAC ACCACTCTCC CTGCCTGTCA GTCTTGGAGA 50

55 TCAGGCCTCC ATCTCTTGCA GATCTAGTCA GAGCCTTGTA CACGGTATTG 100

GAAACACCTA TTTACATTGG TACCTGCAGA AGCCAGGCCA GTCTCCAAAG 150
 CTCCTGATCT ACAAAGTTTC CAACCGATTT TCTGGGGTCC CAGACAGGTT 200
 5 CAGTGGCAGT GGATCAGGGA CAGATTTTCAC ACTCAGGATC AGCAGAGTGG 250
 AGGCTGAGGA TCTGGGACTT TATTTCTGCT CTCAAAGTAC ACATGTTCCG 300
 CTCACGTTTCG GTGCTGGGAC CAAGCTGGAG CTGAAACGGG CTGATGCTGC 350
 10 ACCAACTGTA TCCATCTTCC CACCATCCAG TGAGCAATTG A 391

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	1	5	10	15
Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	20	25	30	
His	Gly	Ile	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	35	40	45	
Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	50	55	60	
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	65	70	75	
Phe	Thr	Leu	Arg	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Leu	80	85	90	
Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Leu	Thr	Phe	Gly	Ala	95	100	105	
Gly	Thr	Lys	Leu	Glu	Leu	Lys	Arg	Ala	Asp	Ala	Ala	Pro	Thr	Val	110	115	120	
Ser	Ile	Phe	Pro	Pro	Ser	Ser	Glu	Gln	Leu	Lys					125	130	131	

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAGATTCAGC TGCAGCAGTC TGGACCTGAG CTGATGAAGC CTGGGGCTTC 50
 AGTGAAGATA TCCTGCAAGG CTTCTGGTTA TTCATTCACT AGCCACTACA 100
 TGCACCTGGGT GAAGCAGAGC CATGGAAAGA GCCTTGAGTG GATTGGCTAC 150
 ATTGATCCTT CCAATGGTGA AACTACTTAC AACCAGAAAT TCAAGGGCAA 200
 GGCCACATTG ACTGTAGACA CATCTCCAG CACAGCCAAC GTGCATCTCA 250
 GCAGCCTGAC ATCTGATGAC TCTGCAGTCT ATTTCTGTGC AAGAGGGGAC 300
 TATAGATACA ACGGCGACTG GTTTTTCGAT GTCTGGGGCG CAGGGACCAC 350
 GGTCACCGTC TCCTCCGCCA AAACCGACAG CCCCATCGGT CTATCCGGGC 400
 CCATC 405

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Glu	Ile	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Met	Lys	Pro	Gly	1	5	10	15
Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	20	25	30	
Ser	His	Tyr	Met	His	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Ser	Leu	35	40	45	
Glu	Trp	Ile	Gly	Tyr	Ile	Asp	Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	50	55	60	
Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Thr	Ser	65	70	75	
Ser	Ser	Thr	Ala	Asn	Val	His	Leu	Ser	Ser	Leu	Thr	Ser	Asp	Asp	80	85	90	
Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	Gly	95	100	105	
Asp	Trp	Phe	Phe	Asp	Val	Trp	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	110	115	120	
Ser	Ser	Ala	Lys	Thr	Asp	Ser	Pro	Ile	Gly	Leu	Ser	Gly	Pro	Ile	125	130	135	

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CTTGGTGGAG GCGGAGGAGA CG 22

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAAACGGGCT GTTGCTGCAC CAACTGTATT CATCTTCC 38

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTCACCGTCT CCTCCGCCTC CACCAAGGGC C 31

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTTCTAT 50

TGCTACAAAT GCATACGCTG ATATCGTGAT GACACAGACA CCACTCTCCC 100

TGCCTGTCAG TCTTGAGAT CAGGCCTCCA TCTCTGTCAG ATCTAGTCAG 150

AGCCTTGTTAC ACGGTATTGG AAACACCTAT TTACATTGGT ACCTGCAGAA 200
 GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC AACCGATTTT 250
 CTGGGGTCCC AGACAGGTTC AGTGGCAGTG GATCAGGGAC AGATTTCACA 300
 CTCAGGATCA GCAGAGTGGG GGCTGAGGAT CTGGGACTTT ATTTCTGCTC 350
 TCAAAGTACA CATGTTCCGC TCACGTTTCG TGCTGGGACC AAGCTGGAGC 400
 TGAAACGGGC TGTGCTGCA CCAACTGTAT TCATCTTCCC ACCATCCAGT 450
 GAGCAATTGA AATCTGGAAC TGCCTCTGTT GTGTGCCTGC TGAATAACTT 500
 CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550
 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600
 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650
 CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700
 CAAAGAGCTT CAACAGGGGA GAGTGTAA 729

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Val	Met	Thr	Gln	Thr	20	25	30	
Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	35	40	45	
Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Gly	Ile	Gly	Asn	Thr	Tyr	50	55	60	
Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	65	70	75	
Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	80	85	90	
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Arg	Ile	Ser	Arg	95	100	105	
Val	Glu	Ala	Glu	Asp	Leu	Gly	Leu	Tyr	Phe	Cys	Ser	Gln	Ser	Thr				

	110	115	120
5	His Val Pro Leu Thr Phe Gly Ala Gly 125	Thr Lys Leu Glu Leu Lys 130	
	Arg Ala Val Ala Ala Pro Thr Val Phe 140	Ile Phe Pro Pro Ser Ser 145	150
10	Glu Gln Leu Lys Ser Gly Thr Ala Ser 155	Val Val Cys Leu Leu Asn 160	165
	Asn Phe Tyr Pro Arg Glu Ala Lys Val 170	Gln Trp Lys Val Asp Asn 175	180
15	Ala Leu Gln Ser Gly Asn Ser Gln Glu 185	Ser Val Thr Glu Gln Asp 190	195
	Ser Lys Asp Ser Thr Tyr Ser Leu Ser 200	Ser Thr Leu Thr Leu Ser 205	210
20	Lys Ala Asp Tyr Glu Lys His Lys Val 215	Tyr Ala Cys Glu Val Thr 220	225
	His Gln Gly Leu Ser Ser Pro Val Thr 230	Lys Ser Phe Asn Arg Gly 235	240
	Glu Cys 242		

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 762 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

40 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCTG TTTTCTCTAT 50

TGCTACAAAC GCGTACGCTG AGATTCAGCT GCAGCAGTCT GGACCTGAGC 100

45 TGATGAAGCC TGGGGCTTCA GTGAAGATAT CCTGCAAGGC TTCTGGTTAT 150

TCATTCAGTA GCCACTACAT GCACTGGGTG AAGCAGAGCC ATGGAAAGAG 200

50 CCTTGAGTGG ATTGGCTACA TTGATCCTTC CAATGGTGAA ACTACTTACA 250

ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC 300

ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA 350

55 TTTCTGTGCA AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG 400

TCTGGGGCGC AGGGACCACG GTCACCGTCT CCTCCGCCTC CACCAAGGGC 450
 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC 500
 5 AGCGGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG 550
 TGTCGTGGAA CTCAGGCGCC CTGACCAGCG GCGTGACAC CTTCCCGGCT 600
 GTCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TGACCGTGCC 650
 10 CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG AATCACAAGC 700
 CCAGCAACAC CAAGGTGGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA 750
 15 ACTCACACAT GA 762

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Ile	Gln	Leu	Gln	Gln	Ser	20	25	30	
Gly	Pro	Glu	Leu	Met	Lys	Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	35	40	45	
Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	Ser	His	Tyr	Met	His	Trp	Val	50	55	60	
Lys	Gln	Ser	His	Gly	Lys	Ser	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asp	65	70	75	
Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	80	85	90	
Ala	Thr	Leu	Thr	Val	Asp	Thr	Ser	Ser	Ser	Thr	Ala	Asn	Val	His	95	100	105	
Leu	Ser	Ser	Leu	Thr	Ser	Asp	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Ala	110	115	120	
Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	Gly	Asp	Trp	Phe	Phe	Asp	Val	Trp	125	130	135	
Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	140	145	150	
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	155	160	165	

	155	160	165
	Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu		
	170	175	180
5	Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val		
	185	190	195
10	His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu		
	200	205	210
	Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr		
	215	220	225
15	Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp		
	230	235	240
	Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr		
	245	250	253

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

30	Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu		
	1	5	10
	Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val		
	20	25	30
35	His Gly Ile Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro		
	35	40	45
40	Gly Gln Ser Pro Lys Leu Leu Ile Tyr Tyr Lys Val Ser Asn Arg		
	50	55	60
	Phe Ser Gly Val Pro Asp Arg Phe Ser Asp Ser Gly Ser Gly Thr		
	65	70	75
45	Asp Phe Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu Gly		
	80	85	90
	Leu Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly		
	95	100	105
50	Ala Gly Thr Lys Leu Glu Leu Lys Arg		
	110	114	

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val
1				5				10						15
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val
				20				25						30
His	Gly	Ile	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro
				35				40						45
Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Tyr	Lys	Val	Ser	Asn	Arg
				50				55						60
Phe	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr
				65				70						75
Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala
				80				85						90
Thr	Tyr	Tyr	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Leu	Thr	Phe	Gly
				95				100						105
Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg						
				110				114						

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: PRT
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val
1				5				10						15
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Lys	Thr	Ile	Ser
				20				25						30
Lys	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys
				35				40						45
Leu	Leu	Ile	Tyr	Tyr	Ser	Gly	Ser	Thr	Leu	Glu	Ser	Gly	Val	Pro
				50				55						60
Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
				65				70						75
Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln
				80				85						90

Gln His Asn Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val
 95 100 105

5 Glu Ile Lys Arg
 109

(2) INFORMATION FOR SEQ ID NO:48:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly
 1 5 10 15

20 Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ser
 20 25 30

Ser His Tyr Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu
 35 40 45

25 Glu Trp Ile Gly Tyr Ile Asp Pro Ser Asn Gly Glu Thr Thr Tyr
 50 55 60

30 Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser
 65 70 75

Ser Ser Thr Ala Asn Val His Leu Ser Ser Leu Thr Ser Asp Asp
 80 85 90

35 Ser Ala Val Tyr Phe Cys Ala Ala Arg Gly Asp Tyr Arg Tyr Asn
 95 100 105

Gly Asp Trp Phe Phe Asp Val Trp Gly Ala Gly Thr
 110 115 117

40 (2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

50 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Phe Ser
 20 25 30

55 Ser His Tyr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

	35	40	45
	Glu Trp Val Gly Tyr Ile Asp Pro Ser Asn Gly Glu Thr Thr Tyr		
	50	55	60
5	Asn Gln Lys Phe Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser		
	65	70	75
10	Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp		
	80	85	90
	Thr Ala Val Tyr Tyr Cys Ala Ala Arg Gly Asp Tyr Arg Tyr Asn		
	95	100	105
15	Gly Asp Trp Phe Phe Asp Val Trp Gly Gln Gly Thr		
	110	115	117

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 amino acids
 (B) TYPE: PRT
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

	Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly		
	1	5	10
30	Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Thr		
	20	25	30
	Gly His Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu		
	35	40	45
35	Glu Trp Val Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Tyr		
	50	55	60
40	Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser		
	65	70	75
	Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp		
	80	85	90
45	Thr Ala Val Tyr Tyr Cys Ala Ala Arg Gly Ile Tyr Phe Tyr Gly		
	95	100	105
	Thr Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr		
	110	115	116

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

5	Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
	Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Gln	Met	Thr	Gln	Ser	20	25	30	
10	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	35	40	45	
	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Gly	Ile	Gly	Asn	Thr	Tyr	50	55	60	
15	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	65	70	75	
	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Ser	Arg	Phe	80	85	90	
20	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	95	100	105	
	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Ser	Gln	Ser	Thr	110	115	120	
25	His	Val	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	125	130	135	
30	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	140	145	150	
	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	155	160	165	
35	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	170	175	180	
40	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	185	190	195	
	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	200	205	210	
45	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	215	220	225	
	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	230	235	240	
50	Glu	Cys														242			

55 (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Val	Gln	Leu	Val	Gln	Ser	20	25	30	
Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	35	40	45	
Ala	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	Ser	His	Tyr	Met	His	Trp	Val	50	55	60	
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Gly	Tyr	Ile	Asp	65	70	75	
Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Arg	80	85	90	
Phe	Thr	Leu	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	95	100	105	
Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	110	115	120	
Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	Gly	Asp	Trp	Phe	Phe	Asp	Val	Trp	125	130	135	
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	140	145	150	
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	155	160	165	
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	170	175	180	
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	185	190	195	
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	200	205	210	
Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	215	220	225	
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	230	235	240	
Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr						

245

250

253

(2) INFORMATION FOR SEQ ID NO:53:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Phe	Asp	Tyr	Glu	Lys	Met
1				5				10						15
Ala	Asn	Ala	Asn	Lys	Gly	Ala	Met	Thr	Glu	Asn	Ala	Asp	Glu	Asn
				20				25						30
Ala	Leu	Gln	Ser	Asp	Ala	Lys	Gly	Lys	Leu	Asp	Ser	Val	Ala	Thr
				35				40						45
Asp	Tyr	Gly	Ala	Ala	Ile	Asp	Gly	Phe	Ile	Gly	Asp	Val	Ser	Gly
				50				55						60
Leu	Ala	Asn	Gly	Asn	Gly	Ala	Thr	Gly	Asp	Phe	Ala	Gly	Ser	Ser
				65				70						75
Asn	Ser	Gln	Met	Ala	Gln	Val	Gly	Asp	Gly	Asp	Asn	Ser	Pro	Leu
				80				85						90
Met	Asn	Asn	Phe	Arg	Gln	Tyr	Leu	Pro	Ser	Leu	Pro	Gln	Ser	Val
				95				100						105
Glu	Cys	Arg	Pro	Phe	Val	Phe	Ser	Ala	Gly	Lys	Pro	Tyr	Glu	Phe
				110				115						120
Ser	Ile	Asp	Cys	Asp	Lys	Ile	Asn	Leu	Phe	Arg	Gly	Val	Phe	Ala
				125				130						135
Phe	Leu	Leu	Tyr	Val	Ala	Thr	Phe	Met	Tyr	Val	Phe	Ser	Thr	Phe
				140				145						150
Ala	Asn	Ile	Leu	Arg	Asn	Lys	Glu	Ser						
				155				159						

45 (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 780 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT 50

TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100
 TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTC AAGTCAA 150
 AGCTTAGTAC ATGGTATAGG TAACACGTAT TTACACTGGT ATCAACAGAA 200
 ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250
 CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300
 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350
 ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400
 TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450
 GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500
 CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550
 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600
 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650
 CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700
 CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750
 CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe
1				5					10					15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Val	Gln	Leu	Val	Glu	Ser
				20					25					30
Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys
				35					40					45
Ala	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	Ser	His	Tyr	Met	His	Trp	Val
				50					55					60
Lys	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Gly	Tyr	Ile	Asp
				65					70					75
Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Arg

	80	85	90
Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln	95	100	105
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala	110	115	120
Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp	125	130	135
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly	140	145	150
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly	155	160	165
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu	170	175	180
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val	185	190	195
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu	200	205	210
Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr	215	220	225
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp	230	235	240
Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr	245	250	253

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe	1	5	10	15
Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser	20	25	30	
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr	35	40	45	
Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Ala Thr Tyr	50	55	60	

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(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 780 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT 50
 TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100
 TGTCCGCCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150
 AGCTTAGTAC ATGGTATAGG TGCTACGTAT TTACACTGGT ATCAACAGAA 200
 ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250
 CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300
 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350
 ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400
 TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450
 GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500
 CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550
 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600
 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650
 CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700
 CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750
 CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 927 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 50

TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAC GCGTACGCTG 100
 AGGTTTCAGCT AGTGCAGTCT GCGGGTGGCC TGGTGCAGCC AGGGGGCTCA 150
 CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC TCCTTCTCGA GTCACTATAT 200
 GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGGATATA 250
 TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT 300
 TTCACCTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA 350
 CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTA CTGTGCA AGAGGGGATT 400
 ATCGCTACAA TGGTGA CTGG TTCTTCGACG TCTGGGGTCA AGGAACCCTG 450
 GTCACCGTCT CCTCGGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 500
 ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG 550
 TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC 600
 CTGACCAGCG GCGTGCACAC CTTCCCCGCT GTCCTACAGT CCTCAGGACT 650
 CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC 700
 AGACCTACAT CTGCAACGTG AATCACAAGC CCAAGCAACAC CAAGGTCGAC 750
 AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCGCCGTG 800
 CCCAGCACCA GAACTGCTGG GCGGCCGCAT GAAACAGCTA GAGGACAAGG 850
 TCGAAGAGCT ACTCTCCAAG AACTACCACC TAGAGAATGA AGTGGCAAGA 900
 CTCAAAAAGC TTGTCGGGGA GCGCTAA 927

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 298 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe
1				5					10					15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Val	Gln	Leu	Val	Gln	Ser
			20					25						30
Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys
			35					40						45
Ala	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	Ser	His	Tyr	Met	His	Trp	Val

	50	55	60
	Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp		
	65	70	75
5	Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg		
	80	85	90
10	Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln		
	95	100	105
	Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala		
	110	115	120
15	Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp		
	125	130	135
	Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly		
	140	145	150
20	Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly		
	155	160	165
25	Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu		
	170	175	180
	Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val		
	185	190	195
30	His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu		
	200	205	210
	Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr		
	215	220	225
35	Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp		
	230	235	240
40	Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro		
	245	250	255
	Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Arg Met Lys Gln Leu		
	260	265	270
45	Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu		
	275	280	285
50	Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg		
	290	295	298

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6563 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

5 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC 50
TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT 100
10 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT 150
TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG 200
GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG 250
15 GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA 300
AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT 350
20 ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GAATTCGAGC 400
TCGGTACCCG GGGATCCTCT CGAGGTTGAG GTGATTTTAT GAAAAAGAAT 450
ATCGCATTTT TTCTTGCATC TATGTTTCGTT TTTTCTATTG CTACAAACGC 500
25 ATACGCTGAT ATCCAGATGA CCCAGTCCCC GAGCTCCCTG TCCGCCTCTG 550
TGGGCGATAG GGTCAACATC ACCTGCAGGT CAAGTCAAAG CTTAGTACAT 600
30 GGTATAGGTG CTACGTATTT AACTGGTAT CAACAGAAAC CAGGAAAAGC 650
TCCGAAACTA CTGATTTACA AAGTATCCAA TCGATTCTCT GGAGTCCCTT 700
CTCGCTTCTC TGGATCCGGT TCTGGGACGG ATTTCACTCT GACCATCAGC 750
35 AGTCTGCAGC CAGAAGACTT CGCAACTTAT TACTGTTTAC AGAGTACTCA 800
TGTCCCCTC ACGTTTGGAC AGGGTACCAA GGTGGAGATC AAACGAACTG 850
40 TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA 900
TCTGGAAGT CTTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA 950
GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAAGTCCC 1000
45 AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC 1050
AGCACCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC 1100
50 CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA 1150
ACAGGGGAGA GTGTTAAGCT GATCCTCTAC GCCGGACGCA TCGTGGCCCT 1200
AGTACGCAAC TAGTCGTAAA AAGGGTATCT AGAGGTTGAG GTGATTTTAT 1250
55 GAAAAAGAAT ATCGCATTTT TTCTTGCATC TATGTTTCGTT TTTTCTATTG 1300

CTACAAACGC GTACGCTGAG GTTCAGCTAG TGCAGTCTGG CGGTGGCCTG 1350
 GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT CTGGCTACTC 1400
 5 CTTCTCGAGT CACTATATGC ACTGGGTCCG TCAGGCCCCG GGTAAGGGCC 1450
 TGGAAATGGGT TGGATATATT GATCCTTCCA ATGGTGAAAC TACGTATAAT 1500
 10 CAAAAGTTCA AGGGCCGTTT CACTTTATCT CGCGACAACT CCAAAAACAC 1550
 AGCATACCTG CAGATGAACA GCCTGCGTGC TGAGGACACT GCCGTCTATT 1600
 ACTGTGCAAG AGGGGATTAT CGCTACAATG GTGACTGGTT CTTCGACGTC 1650
 15 TGGGGTCAAG GAACCCTGGT CACCGTCTCC TCGGCCTCCA CCAAGGGCCC 1700
 ATCGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACCTCT GGGGGCACAG 1750
 20 CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG 1800
 TCGTGGAAC T CAGGCGCCCT GACCAGCGGC GTGCACACCT TCCCGGCTGT 1850
 CCTACAGTCC TCAGGACTCT ACTCCCTCAG CAGCGTGGTG ACCGTGCCCT 1900
 25 CCAGCAGCTT GGGCACCCAG ACCTACATCT GCAACGTGAA TCACAAGCCC 1950
 AGCAACACCA AGGTCGACAA GAAAGTTGAG CCCAAATCTT GTGACAAAAC 2000
 30 TCACACATGC CCGCCGTGCC CAGCACCAGA ACTGCTGGGC GGCCGCATGA 2050
 AACAGCTAGA GGACAAGGTC GAAGAGCTAC TCTCCAAGAA CTACCACCTA 2100
 GAGAATGAAG TGGCAAGACT CAAAAGCTT GTCGGGGAGC GCTAAGCATG 2150
 35 CGACGGCCCT AGAGTCCCTA ACGCTCGGTT GCCGCCGGC GTTTTTTATT 2200
 GTTAACTCAT GTTTGACAGC TTATCATCGA TAAGCTTTAA TGCGGTAGTT 2250
 40 TATCACAGTT AAATTGCTAA CGCAGTCAGG CACCGTGTAT GAAATCTAAC 2300
 AATGCGCTCA TCGTCATCCT CGGCACCGTC ACCCTGGATG CTGTAGGCAT 2350
 AGGCTTGGTT ATGCCGGTAC TGCCGGGCCT CTTGCGGGAT ATCGTCCATT 2400
 45 CCGACAGCAT CGCCAGTCAC TATGGCGTGC TGCTAGCGCT ATATGCGTTG 2450
 ATGCAATTTT TATGCGCACC CGTTCTCGGA GCACTGTCCG ACCGCTTTGG 2500
 50 CCGCCGCCCA GTCCTGCTCG CTTCGCTACT TGGAGCCACT ATCGACTACG 2550
 CGATCATGGC GACCACACCC GTCCTGTGGA TCCTCTACGC CGGACGCATC 2600
 GTGGCCGGCA TCACCGGCGC CACAGGTGCG GTTGCTGGCG CCTATATCGC 2650
 55 CGACATCACC GATGGGGAAG ATCGGGCTCG CCACTTCGGG CTCATGAGCG 2700

CTTGTTTCGG CGTGGGTATG GTGGCAGGCC CCGTGGCCGG GGGACTGTTG 2750
 5 GGCGCCATCT CCTTGACAGC ACCATTCTTT GCGGCGGCGG TGCTCAACGG 2800
 CCTCAACCTA CTAAGGGGCT GCTTCCTAAT GCAGGAGTCG CATAAGGGAG 2850
 AGCGTCGTCC GATGCCCTTG AGAGCCTTCA ACCCAGTCAG CTCCTTCCGG 2900
 10 TGGGCGCGGG GCATGACTAT CGTCGCCGCA CTTATGACTG TCTTCTTTAT 2950
 CATGCAACTC GTAGGACAGG TGCCGGCAGC GCTCTGGGTC ATTTTCGGCG 3000
 AGGACCGCTT TCGCTGGAGC GCGACGATGA TCGGCCTGTC GCTTGCGGTA 3050
 15 TTCGGAATCT TGCACGCCCT CGCTCAAGCC TTCGTCACTG GTCCCGCCAC 3100
 CAAACGTTTC GGCAGAGAAGC AGGCCATTAT CGCCGGCATG GCGGCCGACG 3150
 20 CGCTGGGCTA CGTCTTGCTG GCGTTCGCGA CGCGAGGCTG GATGGCCTTC 3200
 CCCATTATGA TTCTTCTCGC TTCCGGCGGC ATCGGGATGC CCGCGTTGCA 3250
 GGCCATGCTG TCCAGGCAGG TAGATGACGA CCATCAGGGA CAGCTTCAAG 3300
 25 GATCGCTCGC GGCTCTTACC AGCCTAACTT CGATCACTGG ACCGCTGATC 3350
 GTCACGGCGA TTTATGCCGC CTCGGCGAGC ACATGGAACG GGTGCGCATG 3400
 30 GATTGTAGGC GCCGCCCTAT ACCTTGCTCTG CCTCCCCGCG TTGCGTCGCG 3450
 GTGCATGGAG CCGGGCCACC TCGACCTGAA TGGAAGCCGG CGGCACCTCG 3500
 CTAACGGATT CACCACTCCA AGAATTGGAG CCAATCAATT CTTGCGGAGA 3550
 35 ACTGTGAATG CGCAAACCAA CCCTTGGCAG AACATATCCA TCGCGTCCGC 3600
 CATCTCCAGC AGCCGCACGC GGCGCATCTC GGGCAGCGTT GGGTCTTGGC 3650
 40 CACGGGTGCG CATGATCGTG CTCCTGTCTG TGAGGACCCG GCTAGGCTGG 3700
 CGGGGTGACC TTACTGGTTA GCAGAATGAA TCACCGATAC GCGAGCGAAC 3750
 GTGAAGCGAC TGCTGCTGCA AAACGTCTGC GACCTGAGCA ACAACATGAA 3800
 45 TGGTCTTCGG TTTCCGTGTT TCGTAAAGTC TGGAACGCG GAAGTCAGCG 3850
 CCCTGCACCA TTATGTTCCG GATCTGCATC GCAGGATGCT GCTGGCTACC 3900
 50 CTGTGGAACA CCTACATCTG TATTAACGAA GCGCTGGCAT TGACCCTGAG 3950
 TGATTTTTCT CTGGTCCCGC CGCATCCATA CCGCCAGTTG TTTACCCTCA 4000
 CAACGTTCCA GTAACCGGGC ATGTTTCATCA TCAGTAACCC GTATCGTGAG 4050
 55 CATCTCTCT CGTTTCATCG GTATCATTAC CCCCATGAAC AGAAATTCCC 4100

CCTTACACGG AGGCATCAAG TGACCAAACA GGAAAAAACC GCCCTTAACA 4150
 TGGCCCGCTT TATCAGAAGC CAGACATTAA CGCTTCTGGA GAAACTCAAC 4200
 5 GAGCTGGACG CGGATGAACA GGCAGACATC TGTGAATCGC TTCACGACCA 4250
 CGCTGATGAG CTTTACCGCA GCTGCCTCGC GCGTTTCGGT GATGACGGTG 4300
 10 AAAACCTCTG ACACATGCAG CTCCCGGAGA CGGTCACAGC TTGTCTGTAA 4350
 GCGGATGCCG GGAGCAGACA AGCCCGTCAG GCGCGTCAG CGGGTGTGG 4400
 CGGGTGTGGG GCGCAGCCA TGACCCAGTC ACGTAGCGAT AGCGGAGTGT 4450
 15 ATACTGGCTT AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC 4500
 ATATGCGGTG TGAAATACCG CACAGATGCG TAAGGAGAAA ATACCGCATC 4550
 20 AGGCGCTCTT CCGCTTCCTC GCTCACTGAC TCGCTGCGCT CGGTCGTTCC 4600
 GCTGCGGCGA GCGGTATCAG CTCACTCAA GCGGGTAATA CGGTTATCCA 4650
 CAGAATCAGG GGATAACGCA GGAAAGAACA TGTGAGCAAA AGGCCAGCAA 4700
 25 AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT TCCATAGGCT 4750
 CCGCCCCCT GACGAGCATC ACAAATAATCG ACGCTCAAGT CAGAGGTGGC 4800
 30 GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC TGGAAGCTCC 4850
 CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT ACCTGTCCGC 4900
 CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA CGCTGTAGGT 4950
 35 ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG TGTGCACGAA 5000
 CCCCCGTTT AGCCCGACCG CTGCGCCTTA TCCGGTAACT ATCGTCTTGA 5050
 40 GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA GCCACTGGTA 5100
 ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA GTTCTTGAAG 5150
 TGGTGGCCTA ACTACGGCTA CACTAGAAGG ACAGTATTTG GTATCTGCGC 5200
 45 TCTGCTGAAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC TCTTGATCCG 5250
 GCAAACAAAC CACCGCTGGT AGCGGTGGTT TTTTGTGTTG CAAGCAGCAG 5300
 50 ATTACGCGCA GAAAAAAGG ATCTCAAGAA GATCCTTTGA TCTTTTCTAC 5350
 GGGGTCTGAC GCTCAGTGA ACGAAACTC ACGTTAAGGG ATTTTGGTCA 5400
 TGAGATTATC AAAAAGGATC TTCACCTAGA TCCTTTTAAA TTAAAAATGA 5450
 55 AGTTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA 5500

CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTTCGTT 5550
 CATCCATAGT TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG 5600
 5 GGCTTACCAT CTGGCCCCAG TGCTGCAATG ATACCGCGAG ACCCAGCTC 5650
 ACCGGCTCCA GATTTATCAG CAATAAACCA GCCAGCCGGA AGGGCCGAGC 5700
 10 GCAGAAGTGG TCCTGCAACT TTATCCGCCT CCATCCAGTC TATTAATTGT 5750
 TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT 5800
 TGTTGCCATT GCTGCAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG 5850
 15 CTTCAATCAG CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC 5900
 ATGTTGTGCA AAAAAGCGGT TAGCTCCTTC GGTCTCCGA TCGTTGTCAG 5950
 20 AAGTAAGTTG GCCGCAGTGT TATCACTCAT GGTATGGCA GCACTGCATA 6000
 ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT GACTGGTGAG 6050
 TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC 6100
 25 TTGCCCCGCG TCAACACGGG ATAATACCGC GCCACATAGC AGAACTTTAA 6150
 AAGTGCTCAT CATTGGA AAA CGTTCTTCGG GGCGAAAAC CTCAAGGATC 6200
 30 TTACCGCTGT TGAGATCCAG TTCGATGTAA CCCACTCGTG CACCCAACTG 6250
 ATCTTCAGCA TCTTTTACTT TCACCAGCGT TTCTGGGTGA GCAAAAACAG 6300
 GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGTTGA 6350
 35 ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT ATCAGGGTTA 6400
 TTGTCTCATG AGCGGATACA TATTGAATG TATTTAGAAA AATAAACAAA 6450
 40 TAGGGGTTC GCGCACATTT CCCCAGAAAAG TGCCACCTGA CGTCTAAGAA 6500
 ACCATTATTA TCATGACATT AACCTATAAA AATAGGCGTA TCACGAGGCC 6550
 CTTTCGTCTT CAA 6563

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 1 5 10 15

Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser
20 25 30

5 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
35 40 45

Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Glu Thr Tyr
50 55 60

10 Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
65 70 75

15 Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Ser Arg Phe
80 85 90

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
95 100 105

20 Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ser Gln Ser Thr
110 115 120

His Val Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
125 130 135

25 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
140 145 150

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
155 160 165

30 Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
170 175 180

35 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
185 190 195

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
200 205 210

40 Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
215 220 225

45 His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
230 235 240

Glu Cys
242

50 (2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

5 CATGGTATAG GTTAAACTTA TTTACAC 27

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 27 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CATGGTATAG GTNNSACTTA TTTACAC 27

20 (2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 780 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

30 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT 50
TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100
35 TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150
AGCTTAGTAC ATGGTATAGG TGAGACGTAT TTACACTGGT ATCAACAGAA 200
ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250
40 CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300
CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350
45 ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400
TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450
GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500
50 CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550
CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600
55 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650

CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700

CAAAGAGCTT CAACAGGGGA GAGTGTAAAG CTGATCCTCT ACGCCGGACG 750

5 CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTAGTGCAGT CTGGCGGTGG CCTGGTGCAG CCAGGGGGCT CACTCCGTTT 50

GTCCTGTGCA GCTTCTGGCT ACTCCTTC 78

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TCGAGAAGGA GTAGCCAGAA GCTGCACAGG ACAAACGGAG TGAGCCCCCT 50

GGCTGCACCA GGCCACCGCC AGACTGCACT AG 82

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8120 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGATC GACAGCTGTG 50

GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA 100

GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG 150

TCCCCAGGCT CCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA 200

GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC 250

CGCCCAGTTC CGCCCATTCT CCGCCCCATG GCTGACTAAT TTTTTTTATT 300
5 TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG 350
AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAAGCTA GCTTATCCGG 400
CCGGAACGG TGCATTGGAA CGCGGATTCC CCGTGCCAAG AGTGACGTAA 450
10 GTACCGCCTA TAGAGCGATA AGAGGATTTT ATCCCCGCTG CCATCATGGT 500
TCGACCATTG AACTGCATCG TCGCCGTGTC CCAAATATG GGGATTGGCA 550
AGAACGGAGA CCTACCCTGG CCTCCGCTCA GGAACGAGTT CAAGTACTTC 600
15 CAAAGAATGA CCACAACCTC TTCAGTGGAA GGTAAACAGA ATCTGGTGAT 650
TATGGGTAGG AAAACCTGGT TCTCCATTCC TGAGAAGAAT CGACCTTTAA 700
20 AGGACAGAAT TAATATAGTT CTCAGTAGAG AACTCAAAGA ACCACCACGA 750
GGAGCTCATT TTCTTGCCAA AAGTTTGGAT GATGCCTTAA GACTTATTGA 800
ACAACCGGAA TTGGCAAGTA AAGTAGACAT GGTTTGGATA GTCGGAGGCA 850
25 GTTCTGTTTA CCAGGAAGCC ATGAATCAAC CAGGCCACCT TAGACTCTTT 900
GTGACAAGGA TCATGCAGGA ATTTGAAAGT GACACGTTTT TCCCAGAAAT 950
30 TGATTTGGGG AAATATAAAC CTCTCCCAGA ATACCCAGGC GTCCTCTCTG 1000
AGGTCCAGGA GGAAAAAGGC ATCAAGTATA AGTTTGAAGT CTACGAGAAG 1050
AAAGACTAAC AGGAAGATGC TTCAAGTTC TCTGCTCCCC TCCTAAAGCT 1100
35 ATGCATTTTT ATAAGACCAT GGGACTTTTG CTGGCTTTAG ATCCCCTTGG 1150
CTTCGTTAGA ACGCAGCTAC AATTAATACA TAACCTTATG TATCATACAC 1200
40 ATACGATTTA GGTGACACTA TAGATAACAT CCACTTTGCC TTTCTCTCCA 1250
CAGGTGTCCA CTCCCAGGTC CAACTGCACC TCGGTTCTAT CGATTGAATT 1300
CCACCATGGG ATGGTCATGT ATCATCCTTT TTCTAGTAGC AACTGCAACT 1350
45 GGAGTACATT CAGAAGTTCA GCTAGTGCAG TCTGGCGGTG GCCTGGTGCA 1400
GCCAGGGGGC TCACTCCGTT TGTCTGTGTC AGCTTCTGGC TACTCCTTCT 1450
50 CGAGTCACTA TATGCACTGG GTCCGTCAGG CCCCAGGTAA GGGCCTGGAA 1500
TGGGTTGGAT ATATTGATCC TTCCAATGGT GAAACTACGT ATAATCAAAA 1550
GTTCAAGGGC CGTTTCACTT TATCTCGCGA CAACTCCAAA AACACAGCAT 1600
55 ACCTGCAGAT GAACAGCCTG CGTGCTGAGG AACTGCCGT CTATTACTGT 1650

GCAAGAGGGG ATTATCGCTA CAATGGTGAC TGGTTCTTCG ACGTCTGGGG 1700
 TCAAGGAACC CTGGTCACCG TCTCCTCGGC CTCCACCAAG GGCCCATCGG 1750
 TCTTCCCCCT GGCACCCCTC TCCAAGAGCA CCTCTGGGGG CACAGCGGCC 1800
 CTGGGCTGCC TGGTCAAGGA CTA CTCTCCCC GAACCGGTGA CGGTGTCGTG 1850
 GAACTCAGGC GCCCTGACCA GCGGCGTGCA CACCTTCCCG GCTGTCCTAC 1900
 AGTCCTCAGG ACTCTACTCC CTCAGCAGCG TGGTGA CTGT GCCCTCTAGC 1950
 AGCTTGGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA 2000
 CACCAAGGTG GACAAGAAAAG TTGAGCCCAA ATCTTGTGAC AAAACTCACA 2050
 CATGCCCACC GTGCCCAGCA CCTGAACTCC TGGGGGGACC GTCAGTCTTC 2100
 CTCTTCCCCC CAAAACCCAA GGACACCCCTC ATGATCTCCC GGACCCCTGA 2150
 GGTACATGC GTGGTGGTGG ACGTGAGCCA CGAAGACCCT GAGGTCAAGT 2200
 TCAACTGGTA CGTGGACGGC GTGGAGGTGC ATAATGCCAA GACAAAGCCG 2250
 CGGGAGGAGC AGTACAACAG CACGTACCGT GTGGTCAGCG TCCTCACCGT 2300
 CCTGCACCAG GACTGGCTGA ATGGCAAGGA GTACAAGTGC AAGGTCTCCA 2350
 ACAAGCCCT CCCAGCCCCC ATCGAGAAAA CCATCTCCAA AGCCAAAGGG 2400
 CAGCCCCGAG AACCACAGGT GTACACCCCTG CCCCCATCCC GGGAAGAGAT 2450
 GACQAAGAAC CAGGTCAGCC TGACCTGCCT GGTCAAAGGC TTCTATCCCA 2500
 GCGACATCGC CGTGGAGTGG GAGAGCAATG GGCAGCCGGA GAACAACTAC 2550
 AAGACCACGC CTCCCGTGCT GGA CTCCGAC GGCTCCTTCT TCCTCTACAG 2600
 CAAGCTCACC GTGGACAAGA GCAGGTGGCA GCAGGGGAAC GTCTTCTCAT 2650
 GCTCCGTGAT GCATGAGGCT CTGCACAACC ACTACACGCA GAAGAGCCTC 2700
 TCCCTGTCTC CGGGTAAATG AGTGCGACGG CCCTAGAGTC GACCTGCAGA 2750
 AGCTTGGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA 2800
 AATAAAGCAA TAGCATCACA AATTTACAA ATAAAGCATT TTTTTCCTG 2850
 CATTC TAGTT GTGGTTGTC CAACTCATC AATGTATCTT ATCATGTCTG 2900
 GATCGATCGG GAATTAATTC GGCGCAGCAC CATGGCCTGA AATAACCTCT 2950
 GAAAGAGGAA CTTGGTTAGG TACCTTCTGA GGCGGAAAGA ACCATCTGTG 3000
 GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA 3050

GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG 3100
TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA 3150
5 GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC 3200
CGCCCAGTTC CGCCCATTCT CCGCCCCATG GCTGACTAAT TTTTTTTATT 3250
10 TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG 3300
AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAGCTA GCTTATCCGG 3350
CCGGGAACGG TGCATTGGAA CGCGGATTCC CCGTGCCAAG AGTCAGGTAA 3400
15 GTACCGCCTA TAGAGTCTAT AGGCCACCC CTTGGCTTC GTTAGAACGC 3450
GGCTACAATT AATACATAAC CTTTGGATC GATCCTACTG AACTGACAT 3500
20 CCACTTTTTC TTTTCTCCA CAGGTGTCCA CTCCAGGTC CAACTGCACC 3550
TCGGTTGCGG AAGCTAGCTT GGGCTGCATC GATTGAATTC CACCATGGGA 3600
TGGTCATGTA TCATCCTTTT TCTAGTAGCA ACTGCAACTG GAGTACATTC 3650
25 AGATATCCAG ATGACCCAGT CCCCAGCTC CCTGTCCGCC TCTGTGGGCG 3700
ATAGGGTCAC CATCACCTGC AGGTCAAGTC AAAGCTTAGT ACATGGTATA 3750
30 GGTGCTACGT ATTTAACTG GTATCAACAG AAACCAGGAA AAGCTCCGAA 3800
ACTACTGATT TACAAAGTAT CCAATCGATT CTCTGGAGTC CCTTCTCGCT 3850
TCTCTGGATC CGGTTCTGGG ACGGATTTC A CTCTGACCAT CAGCAGTCTG 3900
35 CAGCCAGAAG ACTTCGCAAC TTATTACTGT TCACAGAGTA CTCATGTCCC 3950
GCTCACGTTT GGACAGGGTA CCAAGGTGGA GATCAAACGA ACTGTGGCTG 4000
40 CACCATCTGT CTTATCTTC CCGCATCTG ATGAGCAGTT GAAATCTGGA 4050
ACTGCTTCTG TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA 4100
AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA 4150
45 GTGTCACAGA GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC 4200
CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA 4250
50 AGTCACCCAT CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG 4300
GAGAGTGTTA AGCTTGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT 4350
AATGGTTACA AATAAGCAA TAGCATCACA AATTTACAA ATAAAGCATT 4400
55 TTTTCACTG CATTCTAGTT GTGGTTTGTC CAACTCATC AATGTATCTT 4450

ATCATGTCTG GATCGATCGG GAATTAATTC GGCGCAGCAC CATGGCCTGA 4500
 AATAACCTCT GAAAGAGGAA CTTGGTTAGG TACCTTCTGA GGCGGAAAGA 4550
 5 ACCAGCTGTG GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC 4600
 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG 4650
 10 GTGTGGAAAG TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC 4700
 ATCTCAATTA GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG 4750
 CCCCTAACTC CGCCCAGTTC CGCCCATTCT CCGCCCCATG GCTGACTAAT 4800
 15 TTTTTTTTATT TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC 4850
 AGAAGTAGTG AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAGCTG 4900
 20 TTACCTCGAG CGGCCGCTTA ATTAAGGCGC GCCATTTAAA TCCTGCAGGT 4950
 AACAGCTTGG CACTGGCCGT CGTTTTACAA CGTCGTGACT GGGAAAACCC 5000
 TGGCGTTACC CAACTTAATC GCCTTGCAGC ACATCCCCC TTCGCCAGCT 5050
 25 GCGTAATAG CGAAGAGGCC CGCACCGATC GCCCTTCCCA ACAGTTGCGT 5100
 AGCCTGAATG GCGAATGGCG CCTGATGCGG TATTTTCTCC TTACGCATCT 5150
 30 GTGCGGTATT TCACACCGCA TACGTCAAAG CAACCATAGT ACGCGCCCTG 5200
 TAGCGGCGCA TTAAGCGCGG CGGGTGTGGT GGTTACGCGC AGCGTGACCG 5250
 CTACACTTGC CAGCGCCCTA GCGCCCGCTC CTTTCGCTTT CTTCCCTTCC 5300
 35 TTTCTCGCCA CGTTCGCCGG CTTTCCCCGT CAAGCTCTAA ATCGGGGGCT 5350
 CCCTTTAGGG TTCCGATTTA GTGCTTTACG GCACCTCGAC CCCAAAAAAC 5400
 40 TTGATTTGGG TGATGGTTCA CGTAGTGGG CATCGCCCTG ATAGACGGTT 5450
 TTTCGCCCTT TGACGTTGGA GTCCACGTTT TTTAATAGTG GACTCTTGTT 5500
 CCAAACCTGGA ACAACACTCA ACCCTATCTC GGGCTATTCT TTTGATTTAT 5550
 45 AAGGGATTTT GCCGATTTCG GCCTATTGGT TAAAAAATGA GCTGATTTAA 5600
 CAAAAATTTA ACGCGAATTT TAACAAAATA TTAACGTTTA CAATTTTATG 5650
 50 GTGCACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAACTCC 5700
 GCTATCGCTA CGTGAAGTGG TCATGGCTGC GCGCCGACAC CCGCCAACAC 5750
 CCGCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGGCATC CGCTTACAGA 5800
 55 CAAGCTGTGA CCGTCTCCGG GAGCTGCATG TGTCAGAGGT TTTCACCGTC 5850

ATCACCGAAA CGCGCGAGGC AGTATTCTTG AAGACGAAAG GGCCTCGTGA 5900
TACGCCTATT TTTATAGGTT AATGTCATGA TAATAATGGT TTCTTAGACG 5950
5 TCAGGTGGCA CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT 6000
TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGAT 6050
10 AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT TCAACATTTT 6100
CGTGTGCCCC TTATTCCCTT TTTTGCGGCA TTTTGCCTTC CTGTTTTTGC 6150
15 TCACCCAGAA ACGCTGGTGA AAGTAAAAGA TGCTGAAGAT CAGTTGGGTG 6200
CACGAGTGGG TTACATCGAA CTGGATCTCA ACAGCGGTAA GATCCTTGAG 6250
AGTTTTCGCC CCGAAGAACG TTTTCCAATG ATGAGCACTT TTAAAGTTCT 6300
20 GCTATGTGGC GCGGTATTAT CCCGTGATGA CGCCGGGCAA GAGCAACTCG 6350
GTCGCCGCAT ACACTATTCT CAGAATGACT TGGTTGAGTA CTCACCAGTC 6400
ACAGAAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAT TATGCAGTGC 6450
25 TGCCATAACC ATGAGTGATA ACACTGCGGC CAACTTACTT CTGACAACGA 6500
TCGGAGGACC GAAGGAGCTA ACCGCTTTTT TGCACAACAT GGGGGATCAT 6550
30 GTAACGCGC TTGATCGTTG GGAACCGGAG CTGAATGAAG CCATACCAA 6600
CGACGAGCGT GACACCACGA TGCCAGCAGC AATGGCAACA AC GTTGCGCA 6650
AACTATTAAC TGGCGAACTA CTTACTCTAG CTTCCCGGCA ACAATTAATA 6700
35 GACTGGATGG AGGCGGATAA AGTTGCAGGA CCACTTCTGC GCTCGGCCCT 6750
TCCGGCTGGC TGGTTTATTG CTGATAAATC TGGAGCCGGT GAGCGTGGGT 6800
40 CTCGCGGTAT CATTGCAGCA CTGGGGCCAG ATGGTAAGCC CTCCCGTATC 6850
GTAGTTATCT ACACGACGGG GAGTCAGGCA ACTATGGATG AACGAAATAG 6900
ACAGATCGCT GAGATAGGTG CCTCACTGAT TAAGCATTGG TAACTGTCAG 6950
45 ACCAAGTTTA CTCATATATA CTTTAGATTG ATTTAAAACT TCATTTTAA 7000
TTTAAAAGGA TCTAGGTGAA GATCCTTTTT GATAATCTCA TGACCAAAT 7050
50 CCCTTAACGT GAGTTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA 7100
TCAAAGGATC TTCTTGAGAT CCTTTTTTTC TGCGCGTAAT CTGCTGCTTG 7150
CAAACAAAAA AACCACCGCT ACCAGCGGTG GTTTGTTTGC CGGATCAAGA 7200
55 GCTACCAACT CTTTTTCCGA AGGTAAGTGG CTTCAGCAGA GCGCAGATAC 7250

CAAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA CTTCAAGAAC 7300
TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAGTGGC 7350
5 TGCTGCCAGT GGCATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT 7400
AGTTACCGGA TAAGGCGCAG CGGTCGGGCT GAACGGGGGG TTCGTGCACA 7450
10 CAGCCCAGCT TGGAGCGAAC GACCTACACC GAACTGAGAT ACCTACAGCG 7500
TGAGCATTTGA GAAAGCGCCA CGCTTCCCGA AGGGAGAAAG GCGGACAGGT 7550
ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG GGAGCTTCCA 7600
15 GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG 7650
ACTTGAGCGT CGATTTTTGT GATGCTCGTC AGGGGGGCGG AGCCTATGGA 7700
20 AAAACGCCAG CAACGCGGCC TTTTACGGT TCCTGGCCTT TTGCTGGCCT 7750
TTTGCTCACA TGTTCCTTCC TGCCTTATCC CCTGATTCTG TGGATAACCG 7800
TATTACCGCC TTTGAGTGAG CTGATACCGC TCGCCGCAGC CGAACGACCG 7850
25 AGCGCAGCGA GTCAGTGAGC GAGGAAGCGG AAGAGCGCCC AATACGCAAA 7900
CCGCCTCTCC CCGCGCGTTG GCCGATTCAT TAATCCAGCT GGCACGACAG 7950
30 GTTTCCTCGAC TGGAAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT 8000
ACCTCACTCA TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT 8050
ATGTTGTGTG GAATTGTGAG CGGATAACAA TTTCACACAG GAAACAGCTA 8100
35 TGACCATGAT TACGAATTAA 8120

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 800 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 50
TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAC GCGTACGCTG 100
AGGTTTCAGCT AGTGCAGTCT GCGGTGGCC TGGTGCAGCC AGGGGGCTCA 150
55 CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC TCCTTCTCGA GTCACATATAT 200

GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGGATATA 250
 TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCCT 300
 5 TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA 350
 CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT 400
 ATCGCTACAA TGGTGA CTGTTTCGACG TCTGGGGTCA AGGAACCCTG 450
 10 GTCACCGTCT CCTCGGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 500
 ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG 550
 15 TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC 600
 CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT 650
 CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC 700
 20 AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTCGAC 750
 AAGAAAGTTG AGCCCCAATC TTGTGACAAA ACTCACACAT GCCCGCCTGA 800

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

35	Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	
	1				5					10					15	
	Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Val	Gln	Leu	Val	Gln	Ser	
					20					25					30	
40	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	
					35					40					45	
	Ala	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	Ser	His	Tyr	Met	His	Trp	Val	
45					50					55					60	
	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Gly	Tyr	Ile	Asp	
					65					70					75	
50	Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Arg	
					80					85					90	
	Phe	Thr	Leu	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	
					95					100					105	
55	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
					110					115					120	

	Arg Gly Asp Tyr	Arg Tyr Asn Gly Asp	Trp Phe Phe Asp Val	Trp
	125		130	135
5	Gly Gln Gly Thr	Leu Val Thr Val Ser	Ser Ala Ser Thr Lys	Gly
	140		145	150
	Pro Ser Val Phe	Pro Leu Ala Pro Ser	Ser Lys Ser Thr Ser	Gly
	155		160	165
10	Gly Thr Ala Ala	Leu Gly Cys Leu Val	Lys Asp Tyr Phe Pro	Glu
	170		175	180
	Pro Val Thr Val	Ser Trp Asn Ser Gly	Ala Leu Thr Ser Gly	Val
15		185	190	195
	His Thr Phe Pro	Ala Val Leu Gln Ser	Ser Gly Leu Tyr Ser	Leu
	200		205	210
20	Ser Ser Val Val	Thr Val Pro Ser Ser	Ser Leu Gly Thr Gln	Thr
	215		220	225
	Tyr Ile Cys Asn	Val Asn His Lys Pro	Ser Asn Thr Lys Val	Asp
	230		235	240
25	Lys Lys Val Glu	Pro Lys Ser Cys Asp	Lys Thr His Thr Cys	Pro
	245		250	255
	Pro			
30	256			

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 452 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

40	Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly	1	5	10	15
45	Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Phe Ser	20	25	30	
	Ser His Tyr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	35	40	45	
50	Glu Trp Val Gly Tyr Ile Asp Pro Ser Asn Gly Glu Thr Thr Tyr	50	55	60	
	Asn Gln Lys Phe Lys Gly Arg Phe Thr Leu Ser Arg Asp Asn Ser	65	70	75	
55	Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp				

	80	85	90
	Thr Ala Val Tyr Tyr Cys Ala Arg Gly Asp Tyr Arg Tyr Asn Gly		
5	95	100	105
	Asp Trp Phe Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val		
	110	115	120
10	Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro		
	125	130	135
	Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu		
	140	145	150
15	Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser		
	155	160	165
	Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln		
20	170	175	180
	Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser		
	185	190	195
25	Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys		
	200	205	210
	Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys		
	215	220	225
30	Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu		
	230	235	240
	Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr		
	245	250	255
35	Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp		
	260	265	270
40	Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp		
	275	280	285
	Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln		
	290	295	300
45	Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His		
	305	310	315
	Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn		
50	320	325	330
	Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys		
	335	340	345
55	Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg		
	350	355	360

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
365 370 375

5 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
380 385 390

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
395 400 405

10 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
410 415 420

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
425 430 435

15 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
440 445 450

20 Gly Lys
452

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

35 Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val
20 25 30

His Gly Ile Gly Ala Thr Tyr Leu His Trp Tyr Gln Gln Lys Pro
35 40 45

40 Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
50 55 60

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
65 70 75

45 Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
80 85 90

50 Tyr Tyr Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly Gln
95 100 105

Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
110 115 120

55 Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
125 130 135

	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys
					140					145					150
5	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln
					155					160					165
	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu
					170					175					180
10	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys
					185					190					195
	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val
15					200					205					210
	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys						
					215				219						